



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/840,243

Source: OIPE

Date Processed by STIC: 5-7-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 09/840,243

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics** The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ **Wrapped Aminos** The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ **Incorrect Line Length** The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☐ **Misaligned Amino Acid Numbering** The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ **Non-ASCII** This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ **Variable Length** Sequence(s) ☐ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ **PatentIn ver. 2.0 "bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) ☐. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ **Skipped Sequences (OLD RULES)** Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ **Skipped Sequences (NEW RULES)** Sequence(s) ☐ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☒ **Use of n's or Xaa's (NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ **Use of "Artificial" (NEW RULES)** Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.
- 12 ☐ **Use of <220>Feature (NEW RULES)** Sequence(s) ☐ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ **PatentIn ver. 2.0 "bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

OIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/840,243

DATE: 05/07/2001
TIME: 17:52:54

Input Set : A:\SEQ LIST 010830-117
Output Set: N:\CRF3\05072001\I840243.raw

3 <110> APPLICANT: NOVIMMUNE SA c/o MEDABIOTECH SA
5 <120> TITLE OF INVENTION: NEW TRANSCRIPTION FACTOR OF MHC CLASS II GENES,
6 SUBSTANCES CAPABLE OF INHIBITING THIS NEW TRANSCRIPTION
7 FACTOR AND MEDICAL USES OF THESE SUBSTANCES
9 <130> FILE REFERENCE: B3991A-GD/LL
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/840,243
C--> 12 <141> CURRENT FILING DATE: 2001-04-24
14 <150> PRIOR APPLICATION NUMBER: 98120085.0
15 <151> PRIOR FILING DATE: 1998-10-24
17 <160> NUMBER OF SEQ ID NOS: 19
19 <170> SOFTWARE: PatentIn Ver. 2.1

Does Not Comply
Corrected Diskette Needed
pp. 1-2

ERRORED SEQUENCES

431 <210> SEQ ID NO: 15
432 <211> LENGTH: (37) → Number of amino acids differ:
433 <212> TYPE: PRT - 37 listed
434 <213> ORGANISM: Homo sapiens - 36 shown
436 <400> SEQUENCE: 15
437 Thr Leu Asp Trp Cys Arg Pro Pro His Pro Gly Lys Arg Ala Arg Glu
438 1 5 10 15
440 Arg Pro Val Ala Gly Gln His Arg Arg Leu His Arg His Cys Gly Ala
441 20 25 30
443 Ala Ala Gly Ala
E--> 444 35 (36) → Missing mandatory <220> to <223>
475 <210> SEQ ID NO: 18 features to explain the "Xaa's" in
476 <211> LENGTH: 220 the sequence.
477 <212> TYPE: PRT
478 <213> ORGANISM: Homo sapiens
480 <400> SEQUENCE: 18
481 Asn Ala Phe Asn Val Phe Thr Phe Val Phe His Leu Ala Glu Cys Asn
482 1 5 10 15
E--> 484 Ile His Thr Ser Pro Ser Pro Gly Ile Gln Val Arg His Val (Xaa) Thr
485 20 25 30
487 Pro Ser Thr Thr Lys His Phe Ser Pro Ile Lys Gln Ser Thr Thr Leu
488 35 40 45
490 Thr Asn Lys His Arg Gly Asn Glu Val Ser Thr Thr Pro Leu Leu Ala
491 50 55 60
493 Asn Ser Leu Ser Val His Gln Leu Ala Ala Gln Gly Glu Met Leu Tyr
494 65 70 75 80
496 Leu Ala Thr Arg Ile Glu Gln Glu Asn Val Ile Asn His Thr Asp Glu
497 85 90 95
499 Glu Gly Phe Thr Pro Leu Met Trp Ala Ala Ala His Gly Gln Ile Ala
500 100 105 110
502 Val Val Glu Phe Leu Leu Gln Asn Gly Ala Asp Pro Gln Leu Leu Gly
503 115 120 125

See #10 on the
Error Summary
sheet.

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/840,243

DATE: 05/07/2001
 TIME: 17:52:54

Input Set : A:\SEQ LIST 010830-117
 Output Set: N:\CRF3\05072001\I840243.raw

505 Lys Gly Arg Glu Ser Ala Leu Ser Leu Ala Cys Ser Lys Gly Tyr Thr
 506 130 135 140
 E--> 508 Asp Ile Val (Xaa) Met Leu Leu Asp Cys Gly Val Asp Val Asn (Xaa) Tyr
 509 145 150 155 160
 511 Asp Trp Asn Gly Gly Thr Pro Leu Leu Tyr Ala Val His Gly Asn His
 512 165 170 175
 514 Val Lys Cys Val Lys Met Leu Leu Glu Ser Gly Ala Asp Pro Thr Ile
 515 180 185 190
 517 Glu Thr Asp Ser Gly Tyr Asn Ser Met Asp Leu Ala Val Ala Leu Gly
 518 195 200 205
 520 Ile Glu Val Phe Asn Arg Leu Leu Ser His Ile Cys
 521 210 215 220

→ See p. 1

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/840,243

DATE: 05/07/2001

TIME: 17:52:55

Input Set : A:\SEQ LIST 010830-117

Output Set: N:\CRF3\05072001\I840243.raw

L:11 M:270 C: Current Application Number differs, Replaced Current Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:444 M:252 E: No. of Seq. differs, <211>LENGTH:Input:37 Found:36 SEQ:15
L:484 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
M:340 Repeated in SeqNo=18